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Revised: July 5, 2002.

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Vladimir I. Kashuba , , , a, b, c, 1, 1, Sergei M. Kvasha^{a, c, 1, 1}, Alexei I. Protopopov^{a, b, 1, 1}, Rinat Z. Gizatullin^a, Alla V. Rynditch^c, Claes Wahlestedt^a, Wyeth W. Wasserman^a and Eugene R. Zabarovsky^{a, b, d}

Received 5 September 2000; revised 19 February 2001; accepted 1 March 2001. Received by J.L. Slightom. Available online 22 May 2001.

Abstract

A novel human potassium channel gene was identified and isolated. The maximal open reading frame encodes a protein of 456 amino acids. The predicted product exhibits 91% amino acid identity to the murine voltage-gated potassium channel protein Kv1.7 (Kcna7), which plays an important role in the repolarization of cell membranes. Based on the high similarity, the human gene has been classified as the ortholog of the mouse Kcna7 and given the name Kv1.7 (KCNA7). A structural prediction identified a pore region characteristic of potassium channels and six membrane-spanning domains. Northern expression analysis revealed the gene is expressed preferentially in skeletal muscle, heart and kidney. However, it is expressed at lower level in other tissues, including liver. A single mRNA isoform was observed, with a size of approximately 4.5 kb. Using fluorescence in situ hybridization, the gene was mapped to chromosomal band 19q13.4 (269.13 cR₃₀₀₀). A genomic sequence was identified in the database from this region, and the KCNA7 gene structure determined. Computational analysis of the genomic sequence reveals the location of a putative promoter and a likely muscle-specific regulatory region. Initial comparison to the published murine Kcna7cDNA suggested a different N-terminal sequence for the human protein, however, further analysis suggests that the original mouse sequence contained an error or an unusual polymorphism.

Author Keywords: NotI-linking clone; Gene structure; Gene mapping

Abbreviations: BAC, bacterial artificial chromosome; EST, expressed sequence tag; FISH, fluorescence in situ hybridization; ORF, open reading frame; PCR, polymerase chain reaction; RACE, rapid amplification of cDNA ends

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Gene

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WFSFELLVRLLVCPSKAIFFKNVMNLIDFVAILPYFVALGTELARQRGVGQAMSLAI
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Rashuba,V.I., Kvasha,S.M., Protopopov,A.I., Gizatullin,R.Z., Rynditch,A.V., Wahlestedt,C., Wasserman,W.W. and Zabarovsky,E.R. Initial isolation and analysis of the human KvI.7 (KCNA7) gene, a member of the voltage-qated potassium channel gene family Gene 268 (1-2), 115-122 (2001)
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Submitted (09-FEB-2001) Kashuba V., Microbiology and Tumorbiology
Center, Karolinska Institute, Box 280, 171 77, SWEDEN
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                                                                                                                                                                                                                                potassium voltage-gated channel,
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Best Local Similarity 100.0%; Pred. No. 2e-31;
Matches 250; Conservative 0; Mismatches 0;
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/map="q13.4"
357. .1727
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IVSNFSYFYHRETEGEEAGMFSHVDTQPCGPLEGKANGGLVDGEVPELPPPLMAPPGK
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Submitted (03-MGG-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 157633)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (27-SEP-2000) DOE Joint Genome Institute, 2800 Mitchell
Live, Walnut Creek, CA 94598, USA
4 (bases 1 to 15763)
DOE Joint Genome Institute and Stanford Human Genome Center.
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Submitted (03-0CT-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Oct 3, 2001 this sequence version replaced gi:10312243.
Draft Sequence Produced by DOE Joint Genome Institute
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Finishing Completed at Stanford Human Genome Center
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Best Local Similarity 100.
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